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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/539,834	01/30/2006	Hisashi Narimatsu	159-89	5006

23117 7590 11/17/2006

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EXAMINER	
RAGHU, GANAPATHIRAM	
ART UNIT	**PAPER NUMBER**
1652	

DATE MAILED: 11/17/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/539,834	NARIMATSU ET AL.	
	Examiner	Art Unit	
	Ganapathirama Raghu	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *30 August 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-23* is/are pending in the application.

4a) Of the above claim(s) *1-12 and 17-23* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *13-16* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *06/17 & 10/11/06* 10/11/05
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *SEQ ALIGN*.

DETAILED ACTION

Claims 1-23 are pending in this application and claims 13-16 are now under consideration for examination. Claims 1-12 and 17-23 are withdrawn as they are drawn to non-elected inventions.

Election/Restrictions

Applicants' election with traverse of Group IV, claims 13-16 and SEQ ID NO: 2 for prosecution in their response dated 30 Aug. 2006 is acknowledged. The traversal is on the grounds there would not be serious burden on the examiner to examine groups I through V and restriction between groups be withdrawn and applicants' have requested for examination of all the claims and furthermore polypeptide sequences of SEQ ID NO: 2, SEQ ID NO: 16 and SEQ ID NO: 17 are related in structure and function. Applicants' arguments have been considered, examiner agrees with the arguments regarding the structure and function relationship of SEQ ID NOs.: 2, 16 and 17, however, respectfully disagrees with the argument that searching all claims is "not a serious burden" for the following reasons. Searching structurally distinct molecules like the polypeptides of groups IV, V (antibody group) and the polynucleotides of group I are not coextensive and involves search of different databases and non-patent literature, as prior to the concomitant isolation and expression of the sequence of interest there may be scientific journal articles devoted solely to the polypeptides which would not have described the polynucleotide and moreover the polypeptides may have been isolated by biochemical means and antibodies against said polypeptides may be derived by different methods, therefore searching for the polypeptide may not necessarily describe or yield search results/articles and publications

concerned with the generation of antibodies. Similarly, searching the polypeptides and the method of use of the polypeptides are not coextensive. Groups IV polypeptides encompasses molecules which are structurally distinct and claimed in terms of variants with a wide ranging percentage sequence identity and amino acid changes to SEQ ID NO: 2, SEQ ID NO: 16, or SEQ ID NO: 17, that involves search of sequence databases and analysis of results, whereas method of use of polypeptides as in groups II-III would involve text search and moreover said process or method of use can be carried out by polypeptides that are similar only in activity but from different source and posses different structural features. Therefore, for the above-cited reasons searching of all claims is a serious search burden and contrary to applicants' argument, the requirement is still deemed proper and is therefore made FINAL.

Priority

Acknowledgment is made of applicant's claim for foreign priority under 35 U.S.C. 119(a)-(d). This application is a 371 PCT/JP03/17030 filed on 12/26/2003 and claims the priority date of Japanese application 2002-38075 filed on 12/27/2002. However, Examiner notes that the English translation for the Japanese application 2002-38075 is not provided.

Information Disclosure Statement

The information disclosure statement (IDS) submitted on 06/17 2005 and 10/11/2005 are in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statement is being considered by the examiner.

Drawings

The drawings are considered for examination purposes only.

Claim Rejections 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 13-16 are rejected under 35 U.S.C. 101 because the claims could read on a non-statutory subject matter. The claims are drawn to an 'A β1,3-N-acetyl-D-glucosaminyltransferase', which could read on product of nature. Claims directed to such matter are considered non-statutory. Examiner suggests amending the claims to recite 'An isolated β1,3-N-acetyl-D-glucosaminyltransferase'' to show the hand of man.

Claim Rejections: 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claim 16 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 16 recites the phrase "...40% identity to SEQ ID NO: 2, SEQ ID NO: 16, or SEQ ID NO: 17, the metes and bounds of the phrase is not clear and the examiner suggests changing the phrase to "...40% sequence identity to SEQ ID NO: 2, SEQ ID NO: 16, or SEQ ID NO: 17. Correction is required.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 13-16 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 13-16 are directed to an isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics. Claims 13-16 are rejected under this section 35 U.S.C. 112, because the claims are directed to a genus of polypeptides with no support in the specification for the structural details associated with the function i.e., an isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics. No description of identifying characteristics of all of the sequences of an isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics has been provided by the applicants in the specification.

No information, beyond the characterization of the β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 has been provided by the applicants, which would indicate that they had possession of the claimed genus of the polypeptides i.e., an isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics. Therefore, one skilled in the art cannot reasonably conclude that applicant had possession of the claimed invention at the time the instant application was filed. Applicant is referred to the revised guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at www.uspto.gov.

Claims 13-16 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17, does not reasonably provide enablement for any isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or

inserted and having said specific activity and biochemical characteristics. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and or use the invention commensurate in scope with the claims.

Factors to be considered in determining whether undue experimentation is required are summarized in *In re Wands* (858 F.2d 731, 8 USPQ 2nd 1400 (Fed. Cir. 1988)) as follows: (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claim(s).

Claims 13-16 are so broad as to encompass for any isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics. The scope of the claims are not commensurate with the enablement provided by the disclosure with regard to the extremely large number of polypeptides and encoding polynucleotides broadly encompassed by the claims. Since the amino acid sequence of a protein encoded by a polynucleotide determines its structural and functional properties, predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired activity requires knowledge and guidance with regard to which amino acids in the protein's sequence and the respective codons in its polynucleotide, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed

knowledge of the ways in which the encoded proteins' structure relates to its function. However, in this case the disclosure is limited to an isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17, but provides no guidance with regard to the making of variants and mutants or with regard to other uses. In view of the great breadth of the claims, amount of experimentation required to make the claimed polypeptides and encoding polynucleotides, the lack of guidance, working examples, and unpredictability of the art in predicting function from a polypeptide primary structure (e.g., see Ngo et al. in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz et al. (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495), the claimed invention would require undue experimentation. As such, the specification fails to teach one of ordinary skill how to use the full scope of the polypeptides encompassed by this claim.

While enzyme isolation techniques, recombinant and mutagenesis techniques are known, and it is not routine in the art to screen for multiple substitutions or multiple modifications as encompassed by the instant claim, the specific amino acid positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions or deletions.

The specification does not support the broad scope of the claims which encompass all modifications to any isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having

specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics, because the specification does not establish: (A) regions of the protein/polynucleotide structure which may be modified without affecting the activity of encoded β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics; (B) the general tolerance of the polypeptide and the polynucleotide encoding β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any amino acid residue or the respective codon in the polynucleotide with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claim broadly including polynucleotides with an enormous number of modifications. The scope of the claim must bear a reasonable correlation with the scope of enablement (*In re Fisher*, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of any isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having

said specific activity and biochemical/biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue. See *In re Wands* 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

Claim Rejections 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 13-16 are rejected under 35 U.S.C. 102(b) as being anticipated by Conklin et al., (US Patent No.: 6,416,988, publication date July 02, 2002). Claims 13-16 are directed to any isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics. Conklin et al., (*supra*) teach the isolation of a polypeptide annotated as β1,3-N-acetyl-D-glucosaminyltransferase (SEQ ID NO: 2) that has 99.8% homology to SEQ ID NO: 2 and SEQ ID NO: 16 and 99.7% homology to SEQ ID NO: 17 of the instant application (see sequence alignment provided). The reference also teaches encoding polynucleotides, vectors, host cells and method of making the polypeptide. Therefore, Conklin et al., anticipate claims 13-16 as written.

Claims 13-16 are rejected under 35 U.S.C. 102(b) as being anticipated by Daffo et al., (WO 02/079449, publication date 10/11/2002 also claiming the priority of US Provisional Application No.: 60/279,619 filed on 03/28/2001). Claims 13-16 are directed to any isolated β1,3-N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics. Daffo et al., (*supra*) teach the isolation of a polypeptide annotated as β1,3-N-acetyl-D-glucosaminyltransferase (SEQ ID NO: 568) that has 100% homology to SEQ ID NO: 17 of the instant application (see sequence alignment provided). The reference also teaches encoding polynucleotides, vectors, host cells and method of making the polypeptide. Therefore, Daffo et al., anticipate claims 13-16 as written.

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 13-16 are rejected under 35 U.S.C. 102(e) as being anticipated by Gendreau et al., (WO 2004/066948 A2, publication date 08/12/2004, claiming priority of US Provisional Application No.: 60/443,484 filed on 01/29/03). Claims 13-16 are directed to any isolated β1,3-

N-acetyl-D-glucosaminyltransferase polypeptide having specific activity and biochemical characteristics and comprising an amino acid sequence having 40%-99% sequence identity to the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 16 or SEQ ID NO: 17 or variants of said sequences in which one or several amino acids are substituted, deleted or inserted and having said specific activity and biochemical characteristics. Gendreau et al., (*supra*) teach the isolation of a polypeptide annotated as β1,3-N-acetyl-D-glucosaminyltransferase (SEQ ID NO: 27) that has 100% homology to SEQ ID NO: 17 of the instant application (see sequence alignment provided). The reference also teaches encoding polynucleotides, vectors, host cells and method of making the polypeptide. Therefore, Gendreau et al., anticipate claims 13-16 as written.

This rejection is made on the basis that no English translation for the Japanese application 2002-38075 has been provided and for examination purposes the priority date granted to the instant application is the priority date of 371 PCT/JP03/17030 filed on 12/26/2003.

Conclusion

None of the claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ganapathirama Raghu whose telephone number is 571-272-4533. The examiner can normally be reached on 8 am - 4.30 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy can be reached on 571-272-0928. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300 for regular communications and for After Final communications.

Any inquiry of a general nature or relating to the status of the application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see

http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Ganapathirama Raghu, Ph.D.
Patent Examiner
Art Unit 1652

Oct. 15, 2006.

REBECCA E PROUTY
PRIMARY EXAMINER
GROUP 1600

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  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRCPKCLLCLSALLTLLGLKVYIEWTSESRLSKAYPSPRGTPPSPTPANPEPTLPANLST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRCPKCLLCLSALLTLLGLKVYIEWTSESRLSKAYPSPRGTPPSPTPANPEPTLPANLST 60

Qy         61 RLGQTIPLPFAYWNQQQWRLGSLPSGDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RLGQTIPLPFAYWNQQQWRLGSLPSGDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLL 120

Qy        121 SAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRL 180

Qy        181 LFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVS 240

Qy        241 FVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGG 300

Qy        301 YPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPA 360

Qy        361 DRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 397
              ||||||||||||||||||||||||||||||||||||||
Db        361 DRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 397
```

102(e) 출원, 제16 청구항

RESULT 2
ADR14769
ID ADR14769 standard; protein; 397 AA.
XX
AC ADR14769;
XX
DT 04-NOV-2004 (first entry)
XX
DE Amino acid sequence of human MAPCAX orthologue #1.
XX
KW adenomatous polyposis coli protein; APC; axin pathway;
KW modifier of APC and axin; MAPCAX; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2004066948-A2.
XX
PD 12-AUG-2004.
XX
PF 28-JAN-2004; 2004WO-US002338.
XX
PR 29-JAN-2003; 2003US-0443484P.
PR 11-FEB-2003; 2003US-0447358P.
PR 10-APR-2003; 2003US-0461789P.
PR 14-MAY-2003; 2003US-0470684P.
PR 19-JUN-2003; 2003US-0479650P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Gendreau SB, Morablanco EL, Lickteig K, Zhang H;
XX
DR WPI; 2004-580849/56.
DR N-PSDB; ADR14743.
XX
PT Identifying a candidate adenomatous polyposis coli protein (APC) and axin
PT pathways modulating agent for treating cancer by contacting an assay
PT system comprising a modifier of APC and axin polypeptide or nucleic acid
PT with a test agent.
XX
PS Example 1; SEQ ID NO 27; 199pp; English.
XX
CC The specification describes a method for identifying a candidate
CC adenomatous polyposis coli protein (APC) and axin pathways modulating
CC agents. The method comprises providing an assay system comprising a
CC modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
CC the assay system with a test agent under conditions where, except for the
CC presence of the test agent, the system provides a reference activity, and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate APC and axin pathways
CC modulating agent. The method is useful in identifying a candidate
CC adenomatous polyposis coli protein (APC) and a pathways modulating agent,
CC which are useful for preparing a composition for diagnosing or treating
CC cancer. The present sequence represents a human orthologue of a
CC Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified
CC using BLAST analysis.
XX
SQ Sequence 397 AA;

  Query Match   100.0%; Score 2135; DB 8; Length 397;
  Best Local Similarity   100.0%; Pred. No. 1.4e-182;
  Matches 397; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRCPKCLLCLSALLTLLGLKVYIEWTSESRLSKAYPSPRGTPPSPTPANPEPTLPANLST 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRCPKCLLCLSALLTLLGLKVYIEWTSESRLSKAYPSPRGTPPSPTPANPEPTLPANLST 60

Qy   61 RLGQTIPLPFAYWNQQQWRLGSLPSGDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RLGQTIPLPFAYWNQQQWRLGSLPSGDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLL 120

Qy   121 SAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRL 180

Qy   181 LFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVS 240

Qy   241 FVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 FVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGG 300

Qy   301 YPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 YPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPA 360

Qy   361 DRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 397
              ||||||||||||||||||||||||||||||||||||||
Db   361 DRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 397

RESULT 3
ADU02349
ID ADU02349 standard; protein; 397 AA.
XX
AC ADU02349;
XX
DT 27-JAN-2005 (first entry)
XX
DE Novel human polypeptide seqid 816.
XX
KW cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc;
KW proliferative disorder; inflammatory disorder; immune disorder;
KW metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
KW ulcerative colitis; human.
XX
OS Homo sapiens.
XX
PN WO2004093804-A2.
XX
PD 04-NOV-2004.
XX
PF 19-APR-2004; 2004WO-US012047.
XX
```
```

```
Qy          1 TSESRLSKAYPSPRGTPPSPTPANPEPTLPANLSTRLGQTIPLPFAYWNQQQWRLGSLPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TSESRLSKAYPSPRGTPPSPTPANPEPTLPANLSTRLGQTIPLPFAYWNQQQWRLGSLPS 60

Qy         61 GDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGGSQVSSCSDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGGSQVSSCSDT 120

Qy        121 DVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSPVGEAGPDLDSLVAWESRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSPVGEAGPDLDSLVAWESRR 180

Qy        181 YSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 YSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPP 240

Qy        241 ASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPWLLRAAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPWLLRAAA 300

Qy        301 RVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRTADHCAFRNLLLVRPLGPQASIR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRTADHCAFRNLLLVRPLGPQASIR 360

Qy        361 LWKQLQDPRLQC 372
              ||||||||||||
Db        361 LWKQLQDPRLQC 372
```

RESULT 2
ADQ75983
ID ADQ75983 standard; protein; 397 AA.
XX
AC ADQ75983;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human glycosyl transferase protein.
XX
KW enzyme; human; cancer; glycosyl transferase.
XX
OS Homo sapiens.
XX
PN WO2004061109-A1.
XX
PD 22-JUL-2004.
XX
PF 26-DEC-2003; 2003WO-JP017030.
XX
PR 27-DEC-2002; 2002JP-00380975.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (FJRE) FUJIREBIO INC.
XX
PI Narimatsu H, Kudo T, Togayachi A, Hiruma T;
XX
DR WPI; 2004-534383/51.
DR N-PSDB; ADQ75982.
XX
PT Novel glycosyltransferase nucleic acid, useful for detecting colon
PT cancer, stomach cancer and rectal cancer.
XX
PS Claim 16; SEQ ID NO 2; 80pp; Japanese.
XX
CC The present invention provides the protein and coding sequence of a human
CC glycosyltransferase. The coding sequence is useful for testing for
CC cancer, detecting the effectiveness of treatment to cancer, and for
CC diagnosing cancer such as stomach cancer, pancreatic cancer, liver
CC cancer, colon cancer and rectal cancer. The present sequence is the human
CC glycosyl transferase protein of the invention.
XX
SQ Sequence 397 AA;

```
  Query Match           100.0%;  Score 1999;  DB 8;  Length 397;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-173;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TSESRLSKAYPSPRGTPPSPTPANPEPTLPANLSTRLGQTIPLPFAYWNQQQWRLGSLPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 TSESRLSKAYPSPRGTPPSPTPANPEPTLPANLSTRLGQTIPLPFAYWNQQQWRLGSLPS 85

Qy         61 GDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGGSQVSSCSDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGGSQVSSCSDT 145

Qy        121 DVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSPVGEAGPDLDSLVAWESRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 DVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSPVGEAGPDLDSLVAWESRR 205

Qy        181 YSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 YSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPP 265

Qy        241 ASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPWLLRAAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 ASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPWLLRAAA 325

Qy        301 RVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRTADHCAFRNLLLVRPLGPQASIR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 RVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRTADHCAFRNLLLVRPLGPQASIR 385

Qy        361 LWKQLQDPRLQC 372
              ||||||||||||
Db        386 LWKQLQDPRLQC 397
```

RESULT 3
ADR14769
ID ADR14769 standard; protein; 397 AA.
XX
AC ADR14769;
XX
DT 04-NOV-2004 (first entry)
XX
DE Amino acid sequence of human MAPCAX orthologue #1.
XX
KW adenomatous polyposis coli protein; APC; axin pathway;
KW modifier of APC and axin; MAPCAX; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2004066948-A2.
XX
PD 12-AUG-2004.
XX
PF 28-JAN-2004; 2004WO-US002338.
XX
PR 29-JAN-2003; 2003US-0443484P.
PR 11-FEB-2003; 2003US-0447358P.
PR 10-APR-2003; 2003US-0461789P.
PR 14-MAY-2003; 2003US-0470684P.
PR 19-JUN-2003; 2003US-0479650P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Gendreau SB, Morablanco EL, Lickteig K, Zhang H;
XX
DR WPI; 2004-580849/56.
DR N-PSDB; ADR14743.
XX
PT Identifying a candidate adenomatous polyposis coli protein (APC) and axin
PT pathways modulating agent for treating cancer by contacting an assay
PT system comprising a modifier of APC and axin polypeptide or nucleic acid
PT with a test agent.
XX

PS Example 1; SEQ ID NO 27; 199pp; English.
XX
CC The specification describes a method for identifying a candidate
CC adenomatous polyposis coli protein (APC) and axin pathways modulating
CC agents. The method comprises providing an assay system comprising a
CC modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
CC the assay system with a test agent under conditions where, except for the
CC presence of the test agent, the system provides a reference activity, and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate APC and axin pathways
CC modulating agent. The method is useful in identifying a candidate
CC adenomatous polyposis coli protein (APC) and a pathways modulating agent,
CC which are useful for preparing a composition for diagnosing or treating
CC cancer. The present sequence represents a human orthologue of a
CC Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified
CC using BLAST analysis.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 1999; DB 8; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.4e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TSESRLSKAYPSPRGTPPSPTPANPEPTLPANLSTRLGQTIPLPFAYWNQQQWRLGSLPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 TSESRLSKAYPSPRGTPPSPTPANPEPTLPANLSTRLGQTIPLPFAYWNQQQWRLGSLPS 85

Qy         61 GDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGGSQVSSCSDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GDSTETGGCQAWGAAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGGSQVSSCSDT 145

Qy        121 DVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSPVGEAGPDLDSLVAWESRR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 DVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSPVGEAGPDLDSLVAWESRR 205

Qy        181 YSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 YSDLLLWDFLDVPFNQTLKDLLLLAWLGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPP 265

Qy        241 ASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPWLLRAAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 ASARSLYLGEVFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPWLLRAAA 325

Qy        301 RVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRTADHCAFRNLLLVRPLGPQASIR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 RVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRTADHCAFRNLLLVRPLGPQASIR 385

Qy        361 LWKQLQDPRLQC 372
              ||||||||||||
Db        386 LWKQLQDPRLQC 397
```

RESULT 4
ADU02349
ID ADU02349 standard; protein; 397 AA.
XX
AC ADU02349;
XX
DT 27-JAN-2005 (first entry)
XX
DE Novel human polypeptide seqid 816.
XX
KW cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc;
KW proliferative disorder; inflammatory disorder; immune disorder;
KW metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
KW ulcerative colitis; human.
XX
OS Homo sapiens.
XX
PN WO2004093804-A2.
XX
PD 04-NOV-2004.
XX
PF 19-APR-2004; 2004WO-US012047.
XX
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
PR 08-SEP-2003; 2003US-0505059P.
XX
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PI Lee E, Hestir K, Chu K, Masuoka L, Williams LT;
XX
DR WPI; 2004-775861/76.
DR N-PSDB; ADU01617.
XX
PT New first nucleic acid molecule comprising a polynucleotide sequence
PT given in the specification, useful in preparing a composition for
PT diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
XX
PS Claim 14; SEQ ID NO 816; 291pp; English.
XX
CC The invention describes a new first nucleic acid molecule comprising a
CC polynucleotide sequence given in the specification. Also described are:
CC an animal injected with the nucleic acid molecule; a second nucleic acid
CC molecule comprising a second polynucleotide sequence that is at least
CC about 70, 80, 90 or 95% homologous to the first nucleic acid molecule or
CC that hybridises to the first polynucleotide sequence under high
CC stringency conditions; a vector comprising the nucleic acid molecule and
CC a promoter that drives the expression of the nucleic acid molecule; a
CC host cell transformed, transfected, transduced or infected with the
CC nucleic acid molecule; a nucleic acid composition comprising a carrier or
CC a buffer and one or more compositions comprising the nucleic acid
CC molecule, vector or host cell; a substantially purified polypeptide; an
CC animal injected with the polypeptide; a polypeptide composition
CC comprising the polypeptide molecule and a carrier or buffer; a cell
CC culture medium comprising the polypeptide or transfected cells
CC transfected with the polynucleotide; making a transformed, transfected,
CC transduced, or infected host cell; synthesising Nanodiscs simultaneously
CC and for synthesising a series of simultaneously-synthesised Nanodiscs
CC sequentially utilising a dynamic system; preparing a hydrophobic protein
CC for determination of crystal structure; immunising a non-human animal;
CC screening for modulators of hydrophobic protein activity; a diagnostic
CC kit; determining the presence of the nucleic acid molecule or its
CC complement; determining the presence of an antibody to the polypeptide in
CC a sample; an antibody specifically recognising, binding to or modulating
CC the biological activity of at least one polypeptide encoded by a nucleic
CC acid molecule or its biologically active fragment; an antibody
CC composition comprising the antibody and a carrier; a bacteriophage, where
CC the antibody is displayed on the bacteriophage; a bacterial cell
CC comprising the bacteriophage; a non-human animal injected with the
CC antibody composition; a host cell that secretes the antibody; making an
CC antibody; diagnosing a disease, disorder, syndrome, or condition
CC comprising cancer, or proliferative, inflammatory, immune, metabolic,
CC bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or
CC conditions in a patient; a modulator composition comprising a modulator
CC and a carrier; gene therapy; prophylactic or therapeutic treatment of a
CC subject; an isolated modified cell comprising at least one first
CC heterologous nucleic acid molecule, where the first heterologous nucleic
CC acid molecule comprises a first polynucleotide sequence that encodes a
CC first polypeptide; a non-human animal deficient in the polypeptide or
CC that over-expresses the polypeptide; isolated tissues derived from the
CC non-human animal; and one or more cells derived from the non-human
CC animal. The nucleic acid is useful in preparing a composition for
CC diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.

CC This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 1508; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.7e-148;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 60
Db 116 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 175

Qy 61 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 120
Db 176 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 235

Qy 121 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 180
Db 236 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 295

Qy 181 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 240
Db 296 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 355

Qy 241 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 282
Db 356 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 397

RESULT 5
ADQ75983
ID ADQ75983 standard; protein; 397 AA.
XX
AC ADQ75983;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human glycosyl transferase protein.
XX
KW enzyme; human; cancer; glycosyl transferase.
XX
OS Homo sapiens.
XX
PN WO2004061109-A1.
XX
PD 22-JUL-2004.
XX
PR 26-DEC-2003; 2003WO-JP017030.
XX
PR 27-DEC-2002; 2002JP-00380975.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (FJRE) FUJIREBIO INC.
XX
PI Narimatsu H, Kudo T, Togayachi A, Hiruma T;
XX
DR WPI; 2004-534383/51.
DR N-PSDB; ADQ75982.
XX
PT Novel glycosyltransferase nucleic acid, useful for detecting colon
PT cancer, stomach cancer and rectal cancer.
XX
PS Claim 16; SEQ ID NO 2; 80pp; Japanese.
XX
CC The present invention provides the protein and coding sequence of a human
CC glycosyltransferase. The coding sequence is useful for testing for
CC cancer, detecting the effectiveness of treatment to cancer, and for
CC diagnosing cancer such as stomach cancer, pancreatic cancer, liver
CC cancer, colon cancer and rectal cancer. The present sequence is the human
CC glycosyl transferase protein of the invention.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 1508; DB 8; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.7e-148;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 60
Db 116 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 175

Qy 61 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 120
Db 176 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 235

Qy 121 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 180
Db 236 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 295

Qy 181 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 240
Db 296 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 355

Qy 241 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 282
Db 356 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 397

RESULT 6
ADR14769
ID ADR14769 standard; protein; 397 AA.
XX
AC ADR14769;
XX
DT 04-NOV-2004 (first entry)
XX
DE Amino acid sequence of human MAPCAX orthologue #1.
XX
KW adenomatous polyposis coli protein; APC; axin pathway;
KW modifier of APC and axin; MAPCAX; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2004066948-A2.
XX
PD 12-AUG-2004.
XX
PF 28-JAN-2004; 2004WO-US002338.
XX
PR 29-JAN-2003; 2003US-0443484P.
PR 11-FEB-2003; 2003US-0447358P.

PR 10-APR-2003; 2003US-0461789P.
PR 14-MAY-2003; 2003US-0470684P.
PR 19-JUN-2003; 2003US-0479650P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Gendreau SB, Morablanco EL, Lickteig K, Zhang H;
XX
DR WPI; 2004-580849/56.
DR N-PSDB; ADR14743.
XX
PT Identifying a candidate adenomatous polyposis coli protein (APC) and axin
PT pathways modulating agent for treating cancer by contacting an assay
PT system comprising a modifier of APC and axin polypeptide or nucleic acid
PT with a test agent.
XX
PS Example 1; SEQ ID NO 27; 199pp; English.
XX
CC The specification describes a method for identifying a candidate
CC adenomatous polyposis coli protein (APC) and axin pathways modulating
CC agents. The method comprises providing an assay system comprising a
CC modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
CC the assay system with a test agent under conditions where, except for the
CC presence of the test agent, the system provides a reference activity, and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate APC and axin pathways
CC modulating agent. The method is useful in identifying a candidate
CC adenomatous polyposis coli protein (APC) and a pathways modulating agent,
CC which are useful for preparing a composition for diagnosing or treating
CC cancer. The present sequence represents a human orthologue of a
CC Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified
CC using BLAST analysis.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 1508; DB 8; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.7e-148;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 175

Qy         61 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 235

Qy        121 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 295

Qy        181 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 355

Qy        241 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 282
              ||||||||||||||||||||||||||||||||||||||||||
Db        356 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 397
```

RESULT 7
ADU02349
ID ADU02349 standard; protein; 397 AA.
XX
AC ADU02349;
XX
DT 27-JAN-2005 (first entry)
XX
DE Novel human polypeptide seqid 816.
XX
KW cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc;
KW proliferative disorder; inflammatory disorder; immune disorder;
KW metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
KW ulcerative colitis; human.
XX
OS Homo sapiens.
XX
PN WO2004093804-A2.
XX
PD 04-NOV-2004.
XX
PF 19-APR-2004; 2004WO-US012047.
XX
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
PR 08-SEP-2003; 2003US-0505059P.
XX
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PI Lee E, Hestir K, Chu K, Masuoka L, Williams LT;
XX
DR WPI; 2004-775861/76.
DR N-PSDB; ADU01617.
XX
PT New first nucleic acid molecule comprising a polynucleotide sequence
PT given in the specification, useful in preparing a composition for
PT diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
XX
PS Claim 14; SEQ ID NO 816; 291pp; English.
XX
CC The invention describes a new first nucleic acid molecule comprising a
CC polynucleotide sequence given in the specification. Also described are:
CC an animal injected with the nucleic acid molecule; a second nucleic acid
CC molecule comprising a second polynucleotide sequence that is at least
CC about 70, 80, 90 or 95% homologous to the first nucleic acid molecule or
CC that hybridises to the first polynucleotide sequence under high
CC stringency conditions; a vector comprising the nucleic acid molecule and
CC a promoter that drives the expression of the nucleic acid molecule; a
CC host cell transformed, transfected, transduced or infected with the
CC nucleic acid molecule; a nucleic acid composition comprising a carrier or
CC a buffer and one or more compositions comprising the nucleic acid
CC molecule, vector or host cell; a substantially purified polypeptide; an
CC animal injected with the polypeptide; a polypeptide composition
CC comprising the polypeptide molecule and a carrier or buffer; a cell
CC culture medium comprising the polypeptide or transfected cells
CC transfected with the polynucleotide; making a transformed, transfected,
CC transduced, or infected host cell; synthesising Nanodiscs simultaneously
CC and for synthesising a series of simultaneously-synthesised Nanodiscs
CC sequentially utilising a dynamic system; preparing a hydrophobic protein
CC for determination of crystal structure; immunising a non-human animal;
CC screening for modulators of hydrophobic protein activity; a diagnostic
CC kit; determining the presence of the nucleic acid molecule or its
CC complement; determining the presence of an antibody to the polypeptide in
CC a sample; an antibody specifically recognising, binding to or modulating
CC the biological activity of at least one polypeptide encoded by a nucleic
CC acid molecule or its biologically active fragment; an antibody
CC composition comprising the antibody and a carrier; a bacteriophage, where
CC the antibody is displayed on the bacteriophage; a bacterial cell
CC comprising the bacteriophage; a non-human animal injected with the
CC antibody composition; a host cell that secretes the antibody; making an
CC antibody; diagnosing a disease, disorder, syndrome, or condition
CC comprising cancer, or proliferative, inflammatory, immune, metabolic,
CC bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or
CC conditions in a patient; a modulator composition comprising a modulator
CC and a carrier; gene therapy; prophylactic or therapeutic treatment of a

For 10/539,834

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Qy          1 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 60

Qy         61 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 120

Qy        121 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 180

Qy        181 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 240

Qy        241 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 282
              ||||||||||||||||||||||||||||||||||||||||||
Db        241 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 282
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RESULT 2
ABU11621
ID ABU11621 standard; protein; 298 AA.
XX
AC ABU11621;
XX
DT 12-FEB-2003 (first entry)
XX
DE Human MDDT polypeptide SEQ ID 568.
XX
KW MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW psoriasis; hepatitis.
XX
OS Homo sapiens.
XX
PN WO200279449-A2.
XX
PD 10-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US009944.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR N-PSDB; ABX34611.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.
XX
PS Claim 27; SEQ ID NO 568; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 298 AA;

102(b) for Seq # 17 Only
100% homology

Query Match 100.0%; Score 1508; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.1e-148;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 RRFLLSAACRSFPQWLPGGGGSQVSSCSDTDVPYLLLAVKSEPGRFAERQAVRETWGSPA 76

Qy         61 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 PGIRLLFLLGSPVGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAWLGRH 136

Qy        121 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPGGPFYVPES 196

Qy        181 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 FFEGGYPAYASGGGYVIAGRLAPWLLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFL 256

Qy        241 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 282
              ||||||||||||||||||||||||||||||||||||||||||
Db        257 TAWPADRTADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC 298
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RESULT 3
ADQ75997
ID ADQ75997 standard; protein; 372 AA.
XX
AC ADQ75997;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human glycosyl transferase protein fragment #1.
XX
KW enzyme; human; cancer; glycosyl transferase.
XX
OS Homo sapiens.
XX
PN WO2004061109-A1.
XX
PD 22-JUL-2004.
XX
PF 26-DEC-2003; 2003WO-JP017030.
XX
PR 27-DEC-2002; 2002JP-00380975.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (FJRE) FUJIREBIO INC.